

#11

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1

SEQUENCE LISTING

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BRAMS, PETER
HEARD, CHERYL

<120> INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
CO-STIMULATORY ANTIGENS

<130> 37003-275681

<140> 09/576,424

<141> 2000-05-22

<150> PCT/US97/19906

<151> 1997-10-29

<150> 08/746,361

<151> 1996-11-08

<150> 08/487,550

<151> 1995-06-07

<160> 12

<170> PatentIn Ver. 2.1

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*This
sequence listing
was not formally
entered.
See
sequencing of
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Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro	
275 280 285	
gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc	912
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val	
290 295 300	
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca	960
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr	
305 310 315 320	
aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc	1008
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val	
325 330 335	
ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc	1056
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys	
340 345 350	
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc	1104
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser	
355 360 365	
aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca	1152
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro	
370 375 380	
tcc ccg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc	1200
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val	
385 390 395 400	
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg	1248
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly	
405 410 415	
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac	1296
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp	
420 425 430	
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg	1344
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp	
435 440 445	
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac	1392
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His	
450 455 460	

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 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 465 470 475

1437

<210> 8
 <211> 478
 <212> PRT
 <213> Homo sapiens

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 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30
 Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
 35 40 45
 Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro
 50 55 60
 Glu Trp Val Gly Phe Ile Arg Asn Lys Pro Asn Gly Gly Thr Thr Glu
 65 70 75 80
 Tyr Ala Ala Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95
 Lys Ser Ile Ala Tyr Leu Gln Met Ser Ser Leu Lys Ile Glu Asp Thr
 100 105 110
 Ala Val Tyr Tyr Cys Thr Thr Ser Tyr Ile Ser His Cys Arg Gly Gly
 115 120 125
 Val Cys Tyr Gly Gly Tyr Phe Glu Phe Trp Gly Gln Gly Ala Leu Val
 130 135 140
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 145 150 155 160
 Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 165 170 175
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 180 185 190
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 195 200 205
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 210 215 220
 Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 225 230 235 240
 Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
305 310 315 320

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
325 330 335

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
340 345 350

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
370 375 380

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

<210> 9

<211> 711

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(708)

<400> 9

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1 5 10 15

ggt gca cga tgt gag tct gtc ctg aca cag ccg ccc tca gtg tct ggg	96
Gly Ala Arg Cys Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly	
20 25 30	
gcc cca ggg cag aag gtc acc atc tcg tgc act ggg agc acc tcc aac	144
Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn	
35 40 45	
att gga ggt tat gat cta cat tgg tac cag cag ctc cca gga acg gcc	192
Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala	
50 55 60	
ccc aaa ctc ctc atc tat gac att aac aag cga ccc tca gga att tct	240
Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser	
65 70 75 80	
gac cga ttc tct ggc tcc aag tct ggt acc gcg gcc tcc ctg gcc atc	288
Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile	
85 90 95	
act ggg ctc cag act gag gat gag gct gat tat tac tgc cag tcc tat	336
Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr	
100 105 110	
gac agc agc ctg aat gct cag gta ttc gga gga ggg acc cgg ctg acc	384
Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr	
115 120 125	
gtc cta ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc	432
Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro	
130 135 140	
tcc tct gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata	480
Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile	
145 150 155 160	
agt gac ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc	528
Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser	
165 170 175	
agc ccc gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc	576
Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser	
180 185 190	
aac aac aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag	624
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln	
195 200 205	
tgg aag tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc	672
Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser	
210 215 220	
acc gtg gag aag aca gtg gcc cct aca gaa tgt tca tga	711
Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser	
225 230 235	

<210> 10
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
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Gly Ala Arg Cys Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly
 20 25 30

Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn
 35 40 45

Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala
 50 55 60

Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser
 65 70 75 80

Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile
 85 90 95

Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr
 100 105 110

Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr
 115 120 125

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
 130 135 140

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
 145 150 155 160

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
 165 170 175

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
 180 185 190

Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
 195 200 205

Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser
 210 215 220

Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 225 230 235

<210> 11
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1428)

<400> 11

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
gtc ctg tcc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tcc atc	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile	
35 40 45	
agc ggt ggt tat ggc tgg ggc tgg atc cgc cag ccc cca ggg aag ggg	192
Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly	
50 55 60	
ctg gag tgg att ggg agt ttc tat agt agt agt ggg aac acc tac tac	240
Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr	
65 70 75 80	
aac ccc tcc ctc aag agt caa gtc acc att tca aca gac acg tcc aag	288
Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys	
85 90 95	
aac cag ttc tcc ctg aag ctg aac tct atg acc gcc gcg gac acg gcc	336
Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala	
100 105 110	
gtg tat tac tgt gtg aga gat cgt ctt ttt tca gtt gtt gga atg gtt	384
Val Tyr Tyr Cys Val Arg Asp Arg Leu Phe Ser Val Val Gly Met Val	
115 120 125	
tac aac aac tgg ttc gat gtc tgg ggc ccg gga gtc ctg gtc acc gtc	432
Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val	
130 135 140	
tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc	480
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser	
145 150 155 160	
tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag	528
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys	
165 170 175	
gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg	576
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu	
180 185 190	
acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc	624
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu	
195 200 205	

tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc	672
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr	
210 215 220	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg	720
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val	
225 230 235 240	
gac aag aaa gca gag ccc aaa tct tgt gac aaa act cac aca tgc cca	768
Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro	
245 250 255	
ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc	816
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe	
260 265 270	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	864
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
275 280 285	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	912
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
290 295 300	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	960
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
305 310 315 320	
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc	1008
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
325 330 335	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1056
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
340 345 350	
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc	1104
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala	
355 360 365	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc ccg	1152
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
370 375 380	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	1200
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
385 390 395 400	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg	1248
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
405 410 415	
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc	1296
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
420 425 430	

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1344
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
435 440 445

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1392
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
450 455 460

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1431
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
465 470 475

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<210> 12
<211> 476
<212> PRT
<213> Homo sapiens
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<400> 12
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
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Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile
35 40 45

Ser Gly Gly Tyr Gly Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly
50 55 60

Leu Glu Trp Ile Gly Ser Phe Tyr Ser Ser Ser Gly Asn Thr Tyr Tyr
65 70 75 80

Asn Pro Ser Leu Lys Ser Gln Val Thr Ile Ser Thr Asp Thr Ser Lys
85 90 95

Asn Gln Phe Ser Leu Lys Leu Asn Ser Met Thr Ala Ala Asp Thr Ala
100 105 110

Val	Tyr	Tyr	Cys	Val	Arg	Asp	Arg	Leu	Phe	Ser	Val	Val	Gly	Met	Val
			115				120					125			

Tyr Asn Asn Trp Phe Asp Val Trp Gly Pro Gly Val Leu Val Thr Val
130 135 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
145 150 155 160

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
165 170 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
180 185 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
195 200 205